

Figure 1.  
HBM haplotype indicated with crosshatch

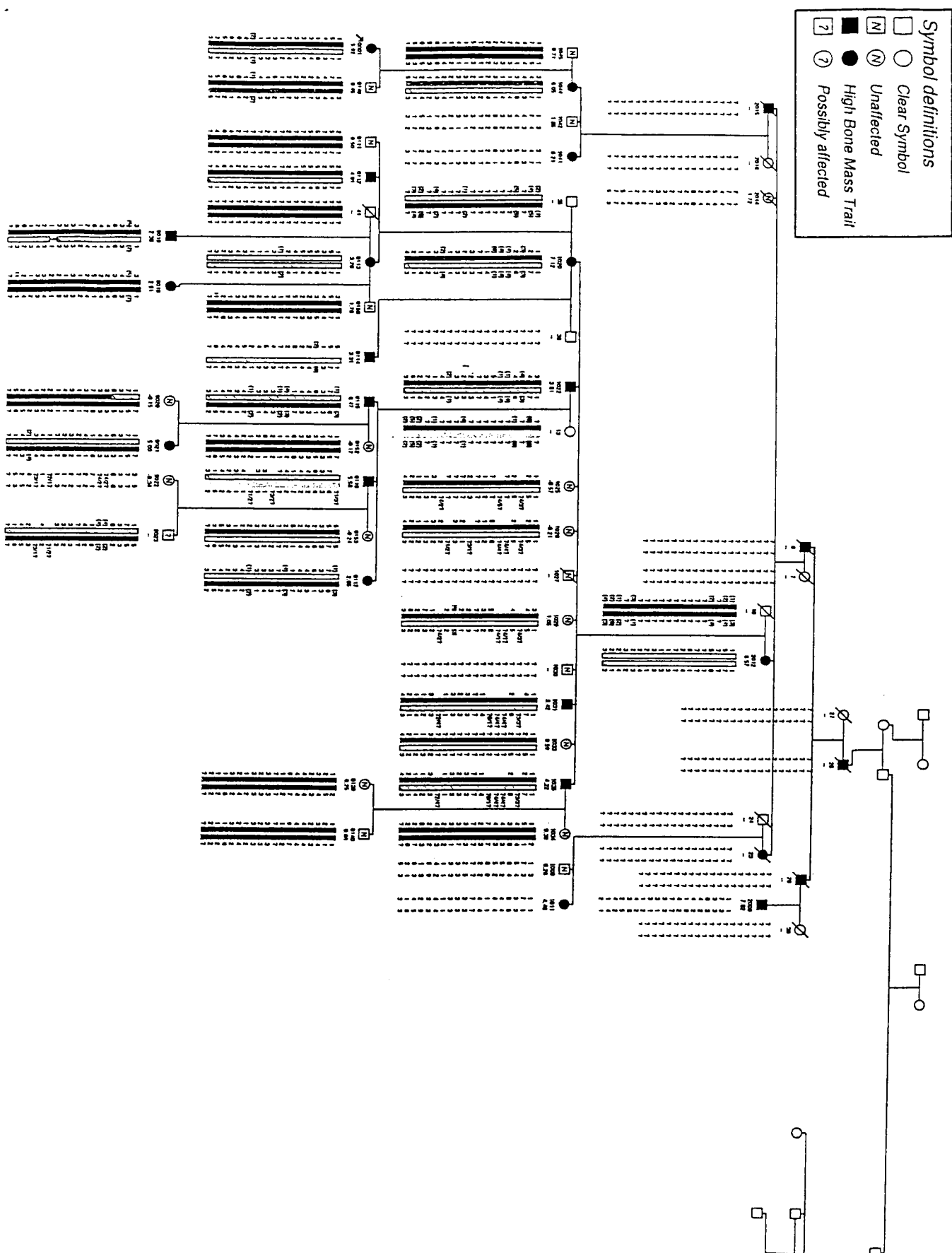


Figure 2

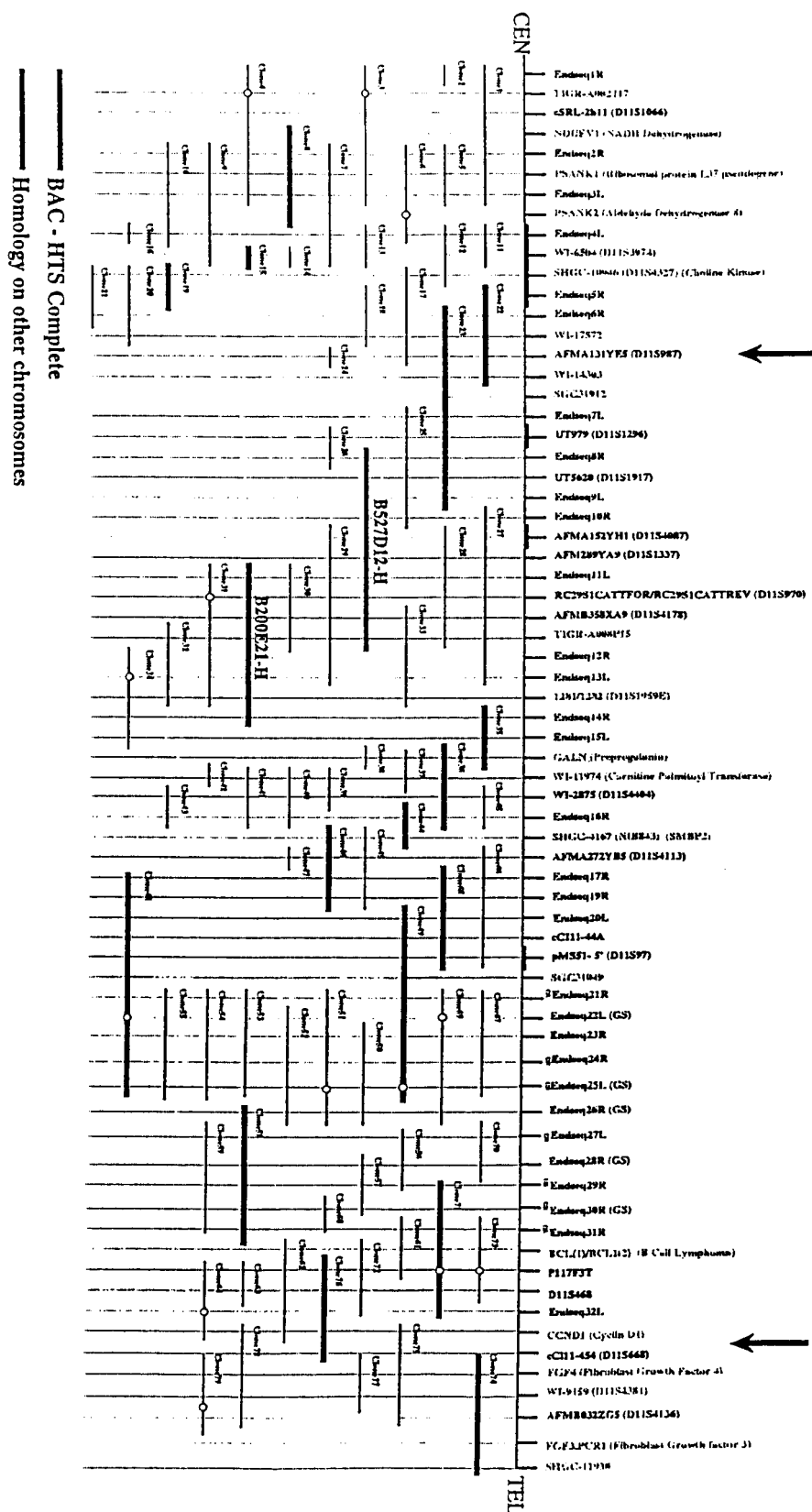
EST/cene

Anonymous STS

STSs from BAC Ends

Genetic Marker

# BAC/STS Map of the HBM Region



**Exon 1**

ACTAAAGCGCCGCGCGCCATGGAGCCCGAGTGAGCGCGGCGCGG  
GCCCCGTCCGGCCGCGGACAACATGGAGGCAGCGCCGCCCCGGGCGCC  
GTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCTGTGCGGCTGC  
CCGGCCCCCGCCGCGGCC

**Exon 2 Coordinates: 527d12\_Contig308G 30944-30549**

gccccacagCCTCGCCGCTCCTGCTATTTGCCAACC GCCGGGACGTACGGCTG  
GTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCATCGTGGTCAGCGGCC  
TGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGTGTA  
CTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAG  
ACGGGGGGCCCGCTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCG  
ACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACTC  
AGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAG  
GTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGCCTTGGACC  
CCGCTCACGGgtaaaccctgctg

... 9408 nt ...

**Exon 3 Coordinates: 527d12\_Contig308G 21141-20945**

ccccgtcacagGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA  
GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGAC  
ATTTACTGGCCCAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCT  
ACTGGGCTGACGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGG  
CTCGTTCCGgtaggtaccac

... 6094 nt ...

**Exon 4 Coordinates: 527d12\_Contig308G 15047-14850**

tccctgactgcagGCAGAAGGTGGTGGAGGGCAGCCTGACGCACCCCTTCGCCC  
TGACGCTCTCCGGGGGACACTCTGTACTGGACAGACTGGCAGACCCGCTC  
CATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTG  
AGTGCCCTATACTACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGC  
AGCCTTTCTgtgagtgcgg

... 1827 nt ...

**Exon 5 Coordinates: 527d12\_Contig308G 13220-13088**

tttctcagTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGCTCCCACCTGT  
GCCTGCTGTCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCACGGG  
TGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGgtgaggcggtgggacg

**FIGURE 3A**

... 20923 nt ...

**Exon 6 Coordinates: 527d12\_Contig309G 7705-8100**

ctccacagGAGCCGAGGAGGTGCTGCTGCTGGCCCCGGCGGACGGACCTACGG  
AGGATCTCGCTGGACACGCCGGAATTCACCGACATCGTGCTGCAGGTGG  
ACGACATCCGGCACGCCATTGCCATCGACTACGACCCGCTAGAGGGGCTA  
TGTCTACTGGACAGATGACGAGGTGCGGGCCATCCGCAGGGCGTACCTG  
GACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGACCCCG  
ATGGCATCGCGGTGCGACTGGGTGGCCCCGAAACCTCTACTGGACCGACAC  
GGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAG  
ATCCTGGTGTGCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACC  
CCGTGATGGGgtaagacgggc

..... 3211 nt .....

**Exon 7 Coordinates: 527d12\_Contig309G 11311-11482**

ttcttctccagCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGT  
GTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCT  
CGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTAC  
TGGGGAGACGCCAAGACAGACAAGATCGAGgtgaggctcctgtgg

..... 13445 nt .....

**Exon 8 Coordinates: 527d12\_Contig309G 24927-25143**

ccgtcctgcagGTGATCAATGTTGATGGGACGAAGAGGCGGACCCTCCTGGAG  
GACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCATCTA  
CTGGACTGACTGGCAGCGCCGCGAGCATCGAGCGGGTGCACAAGGTCAAG  
GCCAGCCGGGACGTCATCATTGACCAGCTGCCCCGACCTGATGGGGCTCA  
AAGCTGTGAATGTGGCCAAGGTTCGTCGgtgagtcgggggggtc

....2826 nt .....

**Exon 9 Coordinates: 527d12\_Contig309G 27969-28256**

gttcgcttcagGAACCAACCCGTGTGCGGACAGGAACGGGGGGGTGCAGCCACC  
TGTGCTTCTTCACACCCACGCAACCCGGTGTGGCTGCCCCATCGGCCT  
GGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTG  
GTCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATA  
ACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCT  
GGACTTTGATGTGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGA  
AGgtagcgtgggc

.....3102.....

**FIGURE 3B**

**Exon 10 Coordinates: 527d12\_Contig309G 31358-31582**

cctgctgccagACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCAC  
GTGGTGGAGTTTGGCCTTGACTACCCCGAGGGCATGGCCGTTGACTGGA  
TGGGCAAGAACCTCTACTGGGCCGACACTGGGACCAACAGAATCGAAGT  
GGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTGGAGGGACTTG  
GACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGGgtaagtgttgctgtc

.....1297 nt.....

**Exon 11 Coordinates: 527d12\_Contig309G 32879-33064**

gtgccttcagCTACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTG  
CGGGCCTTCATGGACGGGACCAACTGCATGACGCTGGTGGACAAGGTGG  
GCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCGCCTCTACTG  
GACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGgtgagggcc  
gggct

.....2069 nt.....

**Exon 12 Coordinates: 527d12\_Contig309G 35133-35454**

gtgtcatgcagGTCAGGAGCGGGTCGTGATTGCCGACGATCTCCCGCACCCGT  
TCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTGGAATCTG  
CACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCCTCA  
TCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCTCCTCC  
CGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGGCAGTGTGGGC  
AGCTGTGCCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACA  
CTACACCCTGGACCCCAGCAGCCGCAACTGCAGCCgtaagtgcctcatggt

.....2006 nt.....

**Exon 13 Coordinates: 527d12\_Contig309G 37460-37659**

gcctcctctaCGCCCACCACCTTCTTGCTGTTCAGCCAGAAATCTGCCATCAGT  
CGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCCTGC  
ATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTT  
CATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGAC  
GGGACCCAGgcaggtgccctgtgg

.....6965 nt.....

**FIGURE 3C**

**Exon 14 Coordinates: 527d12\_Contig309G 44624-44832**

ctttgttctacagCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACA  
GGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTG  
GACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAA  
GCCATGGGGGTGGTGTGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATC  
GTCGTCAACGCGGAGCGAGGgtaggaggccaac

.....1404 nt.....

**Exon 15 Coordinates: 527d12\_Contig309G 46236-46427**

ccaccctcccgcagGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGA  
TCGAACGCGCAGCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCAC  
CGGCCTCATCCGCCCTGTGGCCCTGGTGGTGGACAACACACTGGGCAAG  
CTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGAGAGCTGTGACCTGT  
CAGgtacgcgccccgg

.....686 nt.....

**Exon 16 Coordinates: 527d12\_Contig309G 47113-47322**

ggctgcttcagGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGCAGC  
CTCTGGGCCTGACCATCCTTGGCAAGCATCTCTACTGGATCGACCGCCA  
GCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACT  
CGCATCCAGGGCCGTGTGCGCCACCTCACTGGCATCCATGCAGTGGAGG  
AAGTCAGCCTGGAGGAGTTCTgtacgtgggggc

.....3884 nt.....

**Exon 17 Coordinates: 527d12\_Contig309G 51206-51331**

ttgtctttgcagCAGCCCACCCATGTGCCCGTGACAATGGTGGCTGCTCCCACAT  
CTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATGCCCAGTCCAC  
CTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGgtaggtgtgacctaggtgc

....3905 nt.....

**Exon 18 Coordinates: 527d12\_Contig309G 55236-55472**

gttctctctgtccctccccagAGCCGCCCACCTGCTCCCCGGACCAGTTTGCATGTGC  
CACAGGGGAGATCGACTGTATCCCCGGGGCCTGGCGCTGTGACGGCTTT  
CCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGTGTGCTCCG  
CCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGACCTGCGCCTGCG  
CTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGTGGACTGT  
GACGgtgaggccctcc

.....3052 nt.....

**FIGURE 3D**

**Exon 19 Coordinates: 527d12\_Contig309G 58524-58634**

tctccttgcagCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTG  
TGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCT  
CCGACGAGCTCATGTGTGgtgagccagctt

.....1448 nt.....

**Exon 20 Coordinates: 527d12\_Contig309G 60082-60319**

gtttgtctctggcagAAATCACCAAGCCGCCCTCAGACGACAGCCCCGGCCCCACAGC  
AGTGCCATCGGGCCCCGTCATTGGCATCATCCTCTCTCTTTCGTCATGGG  
TGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGG  
GCCAACGGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGC  
CCCTCAATTTATAGCCCCGGGCGGTTCCAGCATGGCCCCCTTCACAGgta  
aggagcctgagatatggaa

....1095 nt.....

**Exon 21 Coordinates: 527d12\_Contig309G 61414-61552**

cttccttgcagGCATCGCATGCGGAAAGTCCATGATGAGCTCCGTGAGCCTGA  
TGGGGGGCGGGGGCGGGGTGCCCTCTACGACCGGAACACGTCACAG  
GGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCC  
Ggtgaggggcggg

.....6513 nt.....

**Exon 22 Coordinates: 527d12\_Contig309G 68065-68162**

ttggtctctctcagATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG  
TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACC  
GTACAGgtaggacatcccctgcag

.....2273 nt.....

**FIGURE 3E**

**Exon 23 Coordinates: 527d12\_Contig309G 70435-70901**

tcaaacattccggccactgcgagaccgtacagGCCCTACATCATTCGAGGAATGGCGCCCCC  
GACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGC  
CGCTGGAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACC  
CCTATCCACCCCCACCCACGCCCCACAGCCAGTACCTGTCGGCGGAGGA  
CAGCTGCCCCGCCCTCGCCCCGCCACCGAGAGGAGCTACTTCCATCTCTTC  
CCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACCTCGGCCGGGCCA  
CTCTGGCTTCTCTGTGCCCCTGTAAATAGTTTTAAATATGAACAAAGAAAAAA  
ATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGA  
AATGTGAAGTGTGATGGGGTGGGCAGGGCTGGGAGAAGTTTGTACAGTGGAG  
AAATATTTATAAACTTAATTTTGTAACA

**FIGURE 3F**



Figure 4

Model for a LDL Receptor-Related protein, Zmax1

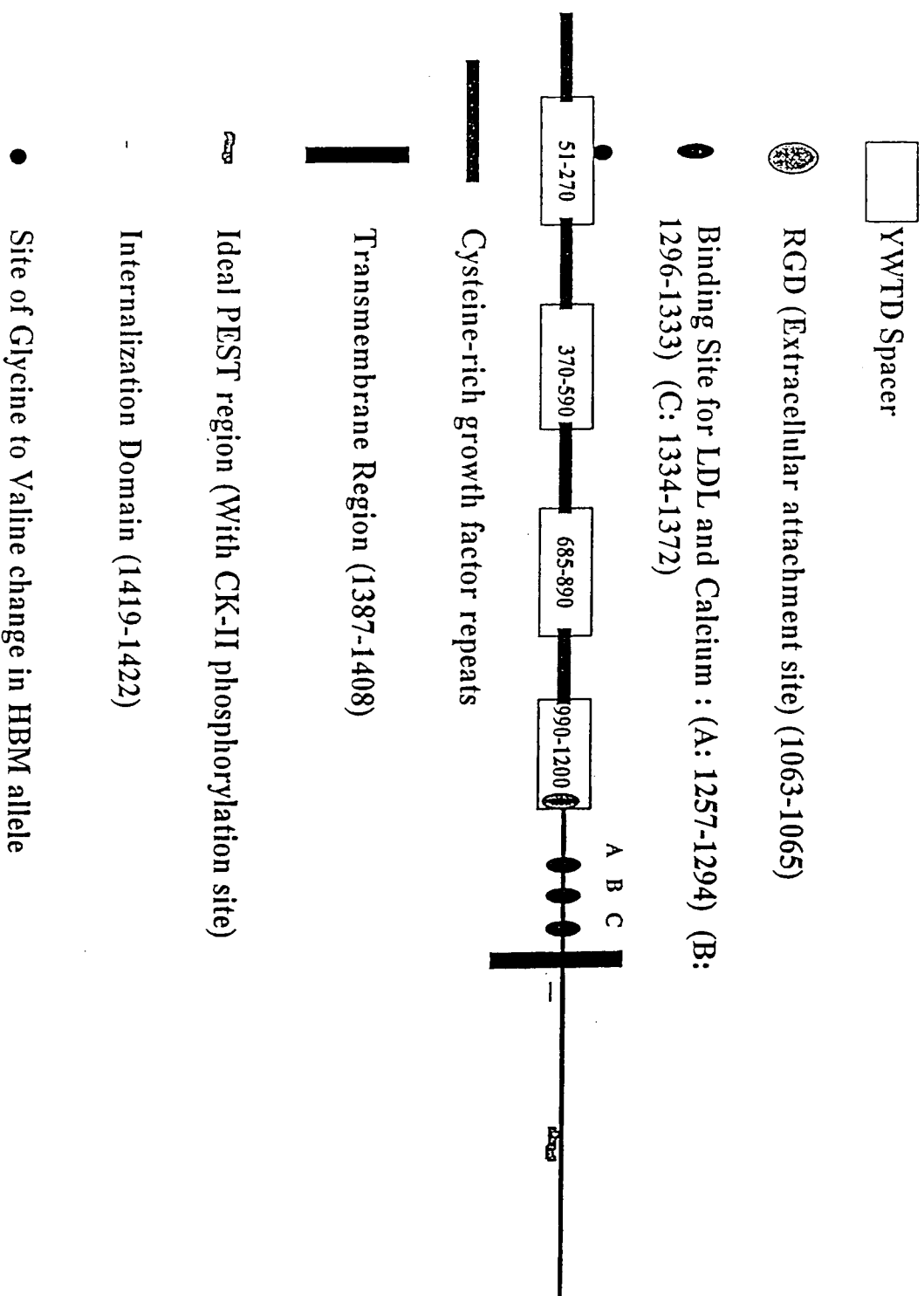
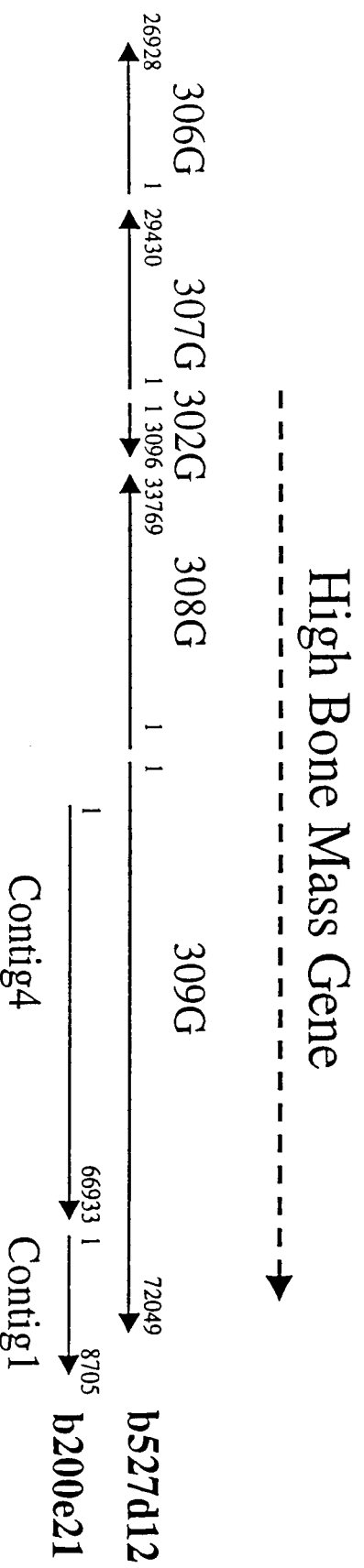


Figure 5



1	ACTAAAGCGCCGCGCGCCATGGAGCCCGAGTGAGCGGCGCGGGCCCGTCCGGCC	60
61	GCCGGACAACATGGAGGCAGCGCCGCGCGCGCGTGGCCGCTGCTGCTGCTGCT	120
1	M E A A P P G P P W P L L L L L L	17
121	GCTGCTGCTGGCGCTGTGCGGCTGCCCCGCCCCCGCGGCGCTCGCCGCTCCTGCTATT	180
18	L L L A L C G C P A P A A A S P L L L F	37
181	TGCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTCCACCAT	240
38	A N R R D V R L V D A G G V K L E S T I	57
241	CGTGGTCAGCGGCGCTGGAGGATGCGGCGCAGTGGACTTCCAGTTTTCCAAGGGAGCCGT	300
58	V V S G L E D A A A V D F Q F S K G A V	77
301	GTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCTACCTGAACCAGACGGGGGC	360
78	Y W T D V S E E A I K Q T Y L N Q T G A	97
361	CGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCTCTCCCGACGGCCTCGCCTGCGACTG	420
98	A V Q N V V I S G L V S P D G L A C D W	117
421	GGTGGGCAAGAAGCTGTACTGGACGGACTCAGAGACCAACCGCATCGAGGTGGCCAACCT	480
118	V G K K L Y W T D S E T N R I E V A N L	137
481	CAATGGCACATCCCGGAAGGTGCTCTTCTGGCAGGACCTTGACCAGCCGAGGGCCATCGC	540
138	N G T S R K V L F W Q D L D Q P R A I A	157
541	CTTGACCCCGCTCACGGGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGA	600
158	L D P A H G Y M Y W T D W G E T P R I E	177
601	GCGGGCAGGGATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCC	660
178	R A G M D G S T R K I I V D S D I Y W P	197
661	CAATGGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTCAG	720
198	N G L T I D L E E Q K L Y W A D A K L S	217
721	CTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAGGGCAGCCT	780
218	F I H R A N L D G S F R Q K V V E G S L	237
781	GACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGGACAGACTGGCAGAC	840
238	T H P F A L T L S G D T L Y W T D W Q T	257
841	CCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAGAGGAAGGAGATCCTGAGTGC	900
258	R S I H A C N K R T G G K R K E I L S A	277
901	CCTCTACTCACCCATGGACATCCAGGTGCTGAGCCAGGAGCGGCAGCCTTTCTTCCACAC	960
278	L Y S P M D I Q V L S Q E R Q P F F H T	297
961	TCGCTGTGAGGAGGACAATGGCGGCTGCTCCACCTGTGCCTGCTGTCCCCAAGCGAGCC	1020
298	R C E E D N G G C S H L C L L S P S E P	317
1021	TTTCTACACATGCGCCTGCCCCACGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAA	1080
318	F Y T C A C P T G V Q L Q D N G R T C K	337
1081	GGCAGGAGCCGAGGAGGTGCTGCTGCTGGCCCCGCGGACGGACCTACGGAGGATCTCGCT	1140
338	A G A E E V L L L A R R T D L R R I S L	357

Figure 6A

1141	GGACACGCCGGACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGGCACGCCATTGC	1200
358	D T P D F T D I V L Q V D D I R H A I A	377
1201	CATCGACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCCAT	1260
378	I D Y D P L E G Y V Y W T D D E V R A I	397
1261	CCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAGATCAACGA	1320
398	R R A Y L D G S G A Q T L V N T E I N D	417
1321	CCCCGATGGCATCGCGGTGCGACTGGGTGGCCCCGAAACCTCTACTGGACCGACACGGGCAC	1380
418	P D G I A V D W V A R N L Y W T D T G T	437
1381	GGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGCAAGATCCTGGTGTCGGAGGA	1440
438	D R I E V T R L N G T S R K I L V S E D	457
1441	CCTGGACGAGCCCCGAGCCATCGCACTGCACCCCGTGATGGGCCTCATGTACTGGACAGA	1500
458	L D E P R A I A L H P V M G L M Y W T D	477
1501	CTGGGGAGAGAACCCTAAAATCGAGTGTGCCAACTTGGATGGGCAGGAGCGGCGTGTGCT	1560
478	W G E N P K I E C A N L D G Q E R R V L	497
1561	GGTCAATGCCTCCCTCGGGTGGCCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCT	1620
498	V N A S L G W P N G L A L D L Q E G K L	517
1621	CTACTGGGGAGACGCCAAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAG	1680
518	Y W G D A K T D K I E V I N V D G T K R	537
1681	GCGGACCCTCCTGGAGGACAAGCTCCCGCACATTTTCGGGTTACGCTGCTGGGGGACTT	1740
538	R T L L E D K L P H I F G F T L L G D F	557
1741	CATCTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGCCAG	1800
558	I Y W T D W Q R R S I E R V H K V K A S	577
1801	CCGGGACGTCATCATTGACCAGCTGCCCCACCTGATGGGGCTCAAAGCTGTGAATGTGGC	1860
578	R D V I I D Q L P D L M G L K A V N V A	597
1861	CAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGTGCAGCCACCTGTGCTT	1920
598	K V V G T N P C A D R N G G C S H L C F	617
1921	CTTCACACCCACGCAACCCGGTGTGGCTGCCCCATCGGCCTGGAGCTGCTGAGTGACAT	1980
618	F T P H A T R C G C P I G L E L L S D M	637
1981	GAAGACCTGCATCGTGCCTGAGGCCTTCTTGGTCTTCACCAGCAGAGCCGCCATCCACAG	2040
638	K T C I V P E A F L V F T S R A A I H R	657
2041	GATCTCCCTCGAGACCAATAACAACGACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGC	2100
658	I S L E T N N N D V A I P L T G V K E A	677
2101	CTCAGCCCTGGACTTTGATGTGTCCAACAACACATCTACTGGACAGACGTCAGCCTGAA	2160
678	S A L D F D V S N N H I Y W T D V S L K	697
2161	GACCATCAGCCGCGCCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCT	2220
698	T I S R A F M N G S S V E H V V E F G L	717

Figure 6B

2221	TGACTACCCCCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACAC	2280
718	D Y P E G M A V D W M G K N L Y W A D T	737
2281	TGGGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTCGTGTG	2340
738	G T N R I E V A R L D G Q F R Q V L V W	757
2341	GAGGGACTTGACAAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGCTACATCTACTG	2400
758	R D L D N P R S L A L D P T K G Y I Y W	777
2401	GACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATGGACGGGACCAACTGCAT	2460
778	T E W G G K P R I V R A F M D G T N C M	797
2461	GACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCTCACCATTGACTACGCTGACCAGCG	2520
798	T L V D K V G R A N D L T I D Y A D Q R	817
2521	CCTCTACTGGACCGACCTGGACACCAACATGATCGAGTCGTCCAACATGCTGGGTCTAGGA	2580
818	L Y W T D L D T N M I E S S N M L G Q E	837
2581	GCGGGTCGTGATTGCCGACGATCTCCCGCACCCGTTCTGGTCTGACGCAGTACAGCGATTA	2640
838	R V V I A D D L P H P F G L T Q Y S D Y	857
2641	TATCTACTGGACAGACTGGAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCG	2700
858	I Y W T D W N L H S I E R A D K T S G R	877
2701	GAACCGCACCCCTCATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCTACTC	2760
878	N R T L I Q G H L D F V M D I L V F H S	897
2761	CTCCCGCCAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTG	2820
898	S R Q D G L N D C M H N N G Q C G Q L C	917
2821	CCTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGACCCAG	2880
918	L A I P G G H R C G C A S H Y T L D P S	937
2881	CAGCCGCAACTGCAGCCCCGCCACACCTTCTTGCTGTTTCAGCCAGAAATCTGCCATCAG	2940
938	S R N C S P P T T F L L F S Q K S A I S	957
2941	TCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTGCCCCTGCATGGACTGAG	3000
958	R M I P D D Q H S P D L I L P L H G L R	977
3001	GAACGTCAAAGCCATCGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCG	3060
978	N V K A I D Y D P L D K F I Y W V D G R	997
3061	CCAGAACATCAAGCGAGCCAAGGACGACGGGACCCAGCCCTTTGTTTTGACCTCTCTGAG	3120
998	Q N I K R A K D D G T Q P F V L T S L S	1017
3121	CCAAGGCCAAAACCCAGACAGGCAGCCCCACGACCTCAGCATCGACATCTACAGCCGGAC	3180
1018	Q G Q N P D R Q P H D L S I D I Y S R T	1037
3181	ACTGTTCTGGACGTGCGAGGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGC	3240
1038	L F W T C E A T N T I N V H R L S G E A	1057
3241	CATGGGGGTGGTGTGCTGCGTGGGGACCGGACAAAGCCAGGGCCATCGTCAACGCGGA	3300
1058	M G V V L R G D R D K P R A I V V N A E	1077

Figure 6C

3301	GCGAGGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCAGC	3360
1078	R G Y L Y F T N M Q D R A A K I E R A A	1097
3361	CCTGGACGGCACCGAGCGCGAGGTCTCTTACCACCGGCCTCATCCGCCCTGTGGCCCT	3420
1098	L D G T E R E V L F T T G L I R P V A L	1117
3421	GGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGACCTGAAGCGCATTGA	3480
1118	V V D N T L G K L F W V D A D L K R I E	1137
3481	GAGCTGTGACCTGTGACGGGGCCAACCGCCTGACCCTGGAGGACGCCAACATCGTGACGCC	3540
1138	S C D L S G A N R L T L E D A N I V Q P	1157
3541	TCTGGGCCTGACCATCCTTGGAAGCATCTCTACTGGATCGACCGCCAGCAGCAGATGAT	3600
1158	L G L T I L G K H L Y W I D R Q Q Q M I	1177
3601	CGAGCGTGTGGAGAAGACCACCGGGGACAAGCGGACTCGCATCCAGGGCCGTGTCGCCCA	3660
1178	E R V E K T T G D K R T R I Q G R V A H	1197
3661	CCTCACTGGCATCCATGCAGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATG	3720
1198	L T G I H A V E E V S L E E F S A H P C	1217
3721	TGCCCCGTGACAATGGTGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACG	3780
1218	A R D N G G C S H I C I A K G D G T P R	1237
3781	GTGCTCATGCCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCC	3840
1238	C S C P V H L V L L Q N L L T C G E P P	1257
3841	CACCTGCTCCCCGACAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGGGGC	3900
1258	T C S P D Q F A C A T G E I D C I P G A	1277
3901	CTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGGCTGCCCCGT	3960
1278	W R C D G F P E C D D Q S D E E G C P V	1297
3961	GTGCTCCGCCGCCAGTTCCCTGCGCGCGGGGTGAGTGTGTGGACCTGCGCCTGCGCTG	4020
1298	C S A A Q F P C A R G Q C V D L R L R C	1317
4021	CGACGGCGAGGCAGACTGTGACGACCGCTCAGACGAGGTGGACTGTGACGCCATCTGCCT	4080
1318	D G E A D C Q D R S D E V D C D A I C L	1337
4081	GCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTGTGTCTCATCAAACAGCAGTGCGACTC	4140
1338	P N Q F R C A S G Q C V L I K Q Q C D S	1357
4141	CTTCCCCGACTGTATCGACGGCTCCGACGAGCTCATGTGTGAAATCACCAAGCCGCCCTC	4200
1358	F P D C I D G S D E L M C E I T K P P S	1377
4201	AGACGACAGCCCGGCCACAGCAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCT	4260
1378	D D S P A H S S A I G P V I G I I L S L	1397
4261	CTTCGTATGGGTGGTGTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGG	4320
1398	F V M G G V Y F V C Q R V V C Q R Y A G	1417
4321	GGCCAACGGGCCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCCTCAATTT	4380
1418	A N G P F P H E Y V S G T P H V P L N F	1437

Figure 6D

4381	CATAGCCCCGGGCGGTTC	CCCAGCATGGCCCCCTT	CACAGGCATCGCATGCGG	AAAAGTCCAT	4440
1438	I A P G G S Q H G P F T G I A C G K S M				1457
4441	GATGAGCTCCGTGAGCCT	GATGGGGGGCCGGGGCGGGG	TGCCCCCTCTACGACCGGAACCA		4500
1458	M S S V S L M G G R G G V P L Y D R N H				1477
4501	CGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACGCTGTACCCGCCGAT				4560
1478	V T G A S S S S S S S S T K A T L Y P P I				1497
4561	CCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTGTACAACATGGACATGTTCTA				4620
1498	L N P P P S P A T D P S L Y N M D M F Y				1517
4621	CTCTTCAAACATTCCGGCCACTGCGAGACCGTACAGGCCCTACATCATTCGAGGAATGGC				4680
1518	S S N I P A T A R P Y R P Y I I R G M A				1537
4681	GCCCCGACGACGCCCTGCAGCACCGACGTGTGTGACAGCGACTACAGCGCCAGCCGCTG				4740
1538	P P T T P C S T D V C D S D Y S A S R W				1557
4741	GAAGGCCAGCAAGTACTACCTGGATTTGAACTCGGACTCAGACCCCTATCCACCCCCACC				4800
1558	K A S K Y Y L D L N S D S D P Y P P P P				1577
4801	CACGCCCCACAGCCAGTACCTGTGCGGCGGAGGACAGCTGCCCCGCCCTCGCCCCGCCACCGA				4860
1578	T P H S Q Y L S A E D S C P P S P A T E				1597
4861	GAGGAGCTACTTCCATCTCTTCCCGCCCCCTCCGTCCCCCTGCACGGACTCATCCTGACC				4920
1598	R S Y F H L F P P P P S P C T D S S				1615
4921	TCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCGTGAAATAGTTTTAAATATGAACAAAGA				4980
4981	AAAAAATATATTTTATGATTTAAAAAATAAATATAATTGGGATTTTAAAAACATGAGAAA				5040
5041	TGTGAACTGTGATGGGGTGGGCAGGGCTGGGAGAACTTTGTACAGTGAGAAATATTTAT				5100
5101	AAACTTAATTTTGTAAACA	5120			

Figure 6E

# Northern Blot Analysis - Zmax 1

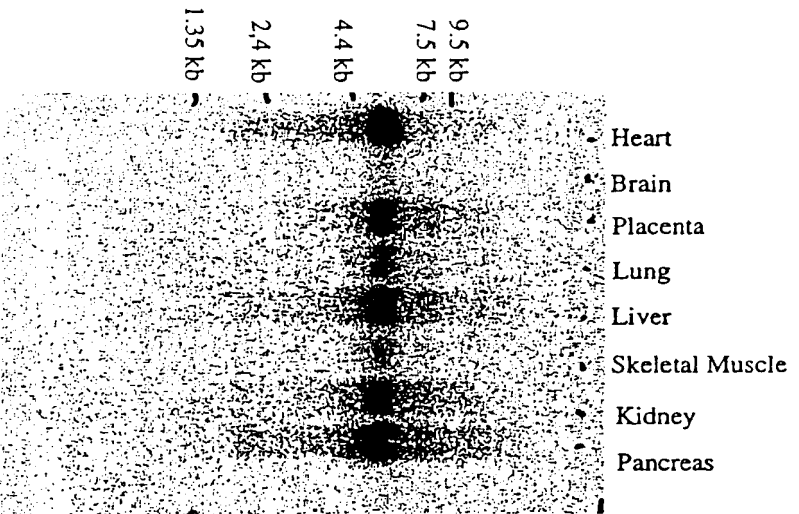


Figure 7A

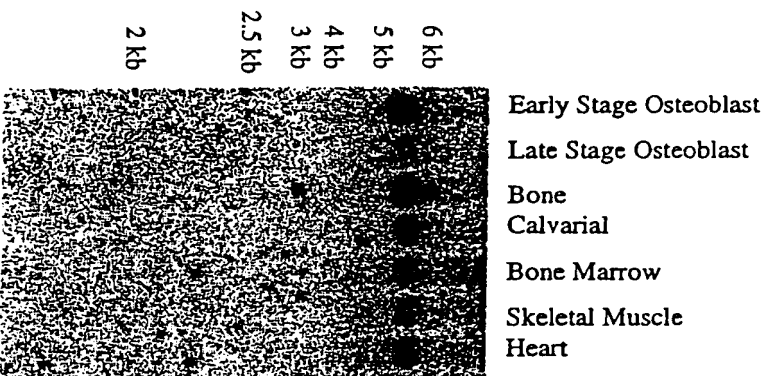


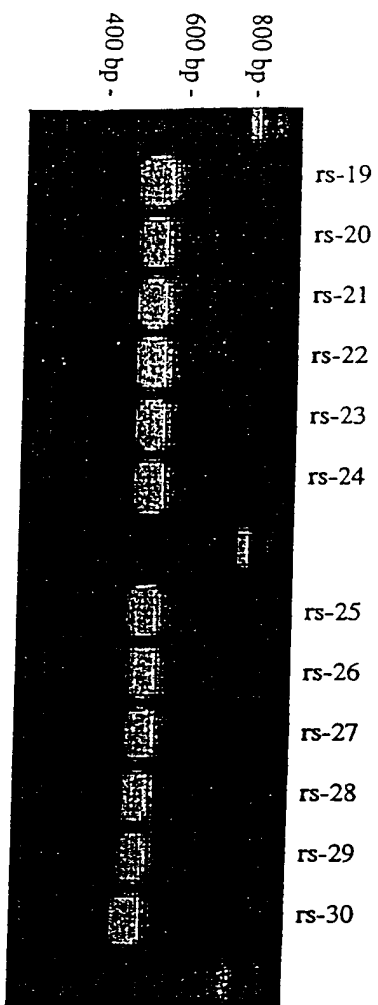
Figure 7B



Figure 8

Zmax 1 random samples

b527dl2-h\_Contig087C\_1.mt



# ASO Detection of the Zmax1 Exon 3 Mutation

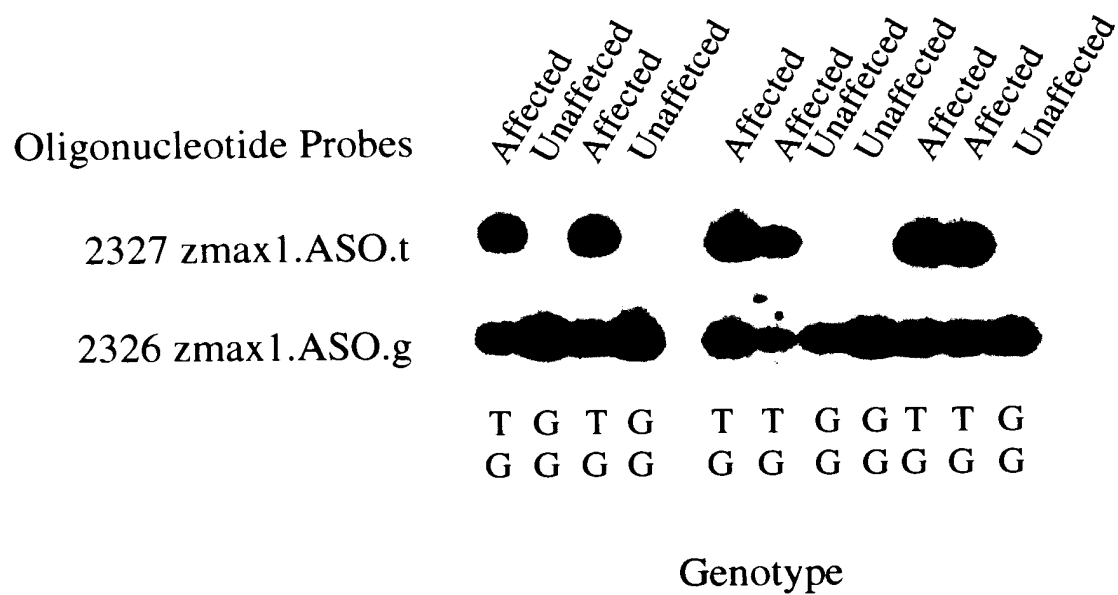
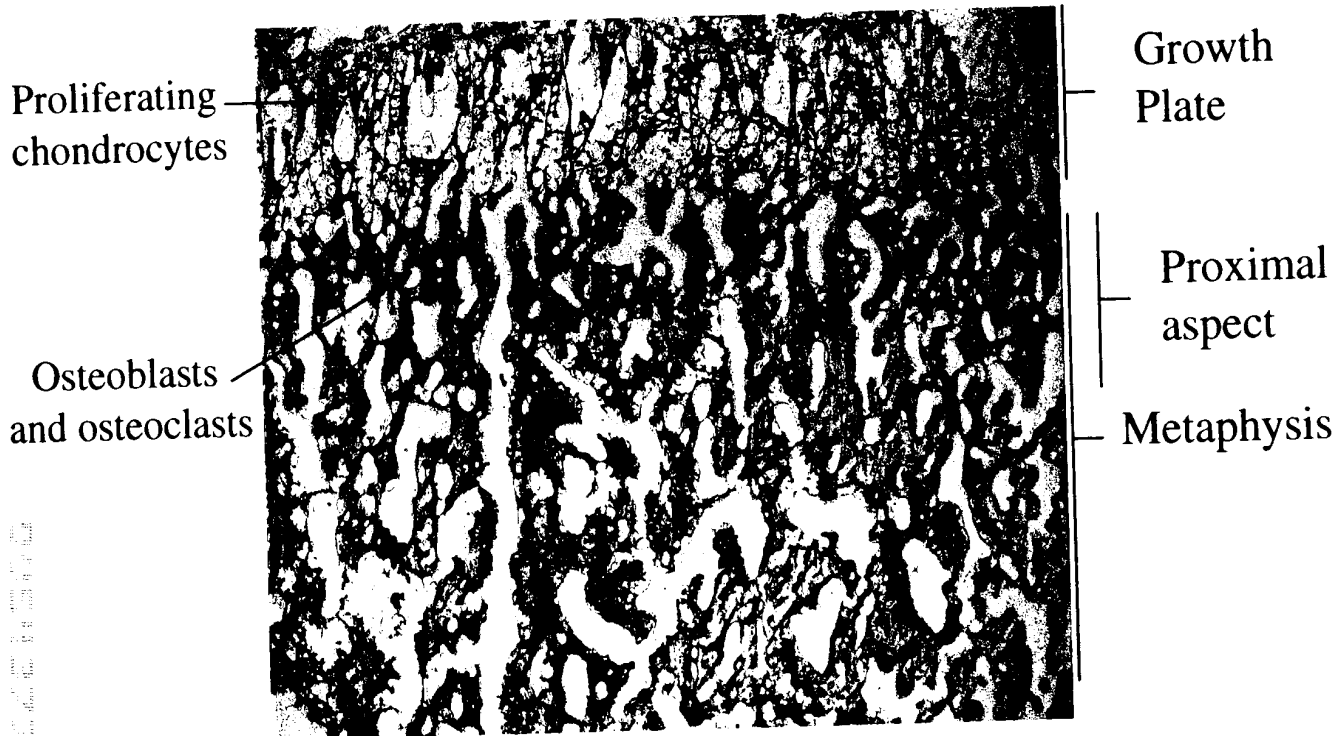


FIG. 9

Mouse Zmax1 In situ hybridization  
100X Magnification

Antisense probe



Sense probe

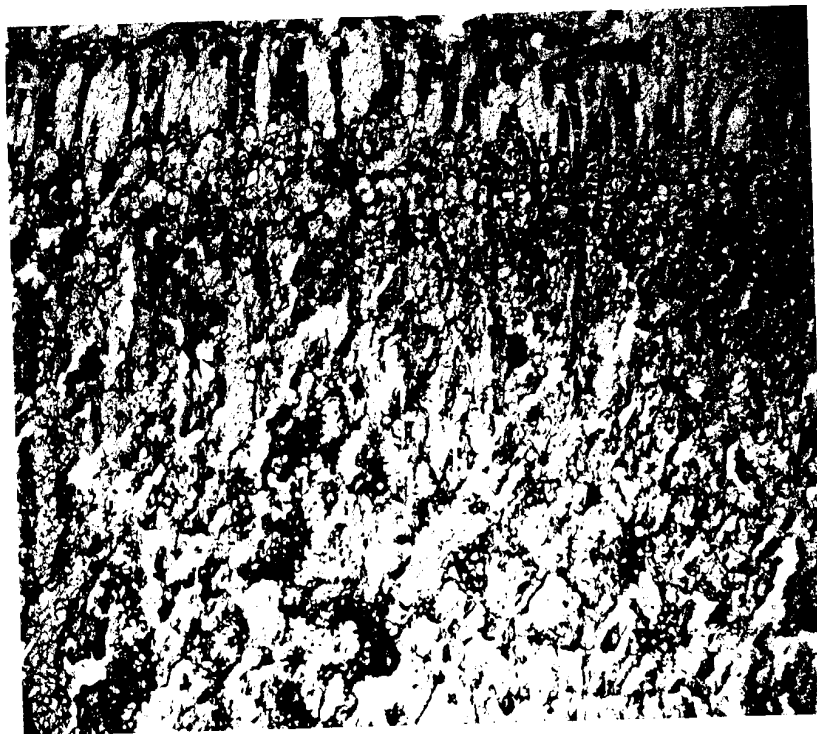


FIG. 10

Mouse Zmax1 In situ hybridization  
400X magnification

Antisense probe

Osteoblasts  
and osteoclasts

Trabecular  
bone

Proximal  
Metaphysis



Sense probe



FIG. 11

Mouse Zmax1 In situ hybridization  
400X magnification

Antisense probe

Osteoblasts

Endosteum



Sense probe

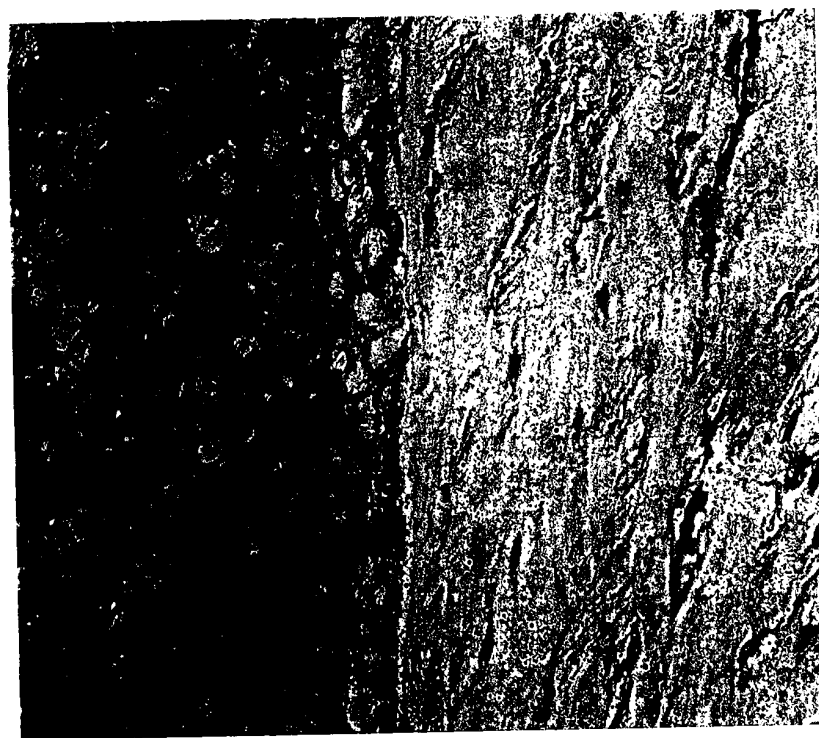
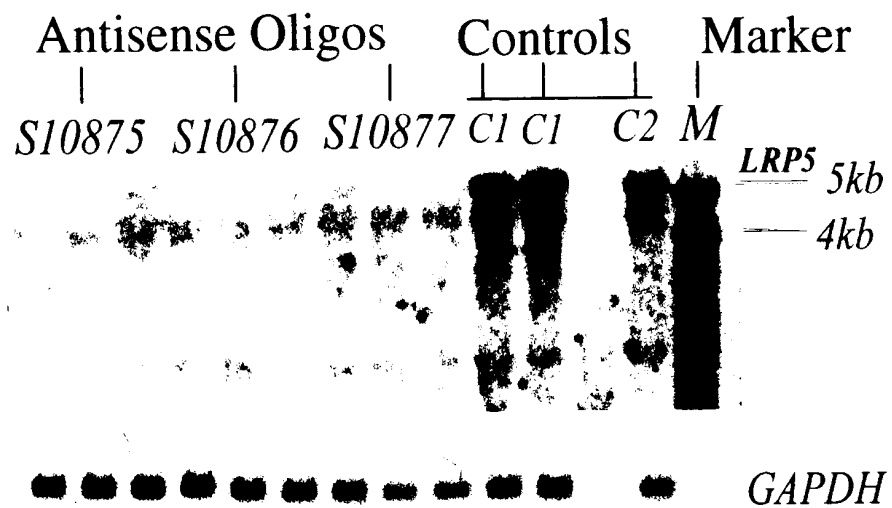


FIG. 12

## Antisense Inhibition of Zmax1 Expression



MC-3T3 cells

FIG. 13